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Supplementary material

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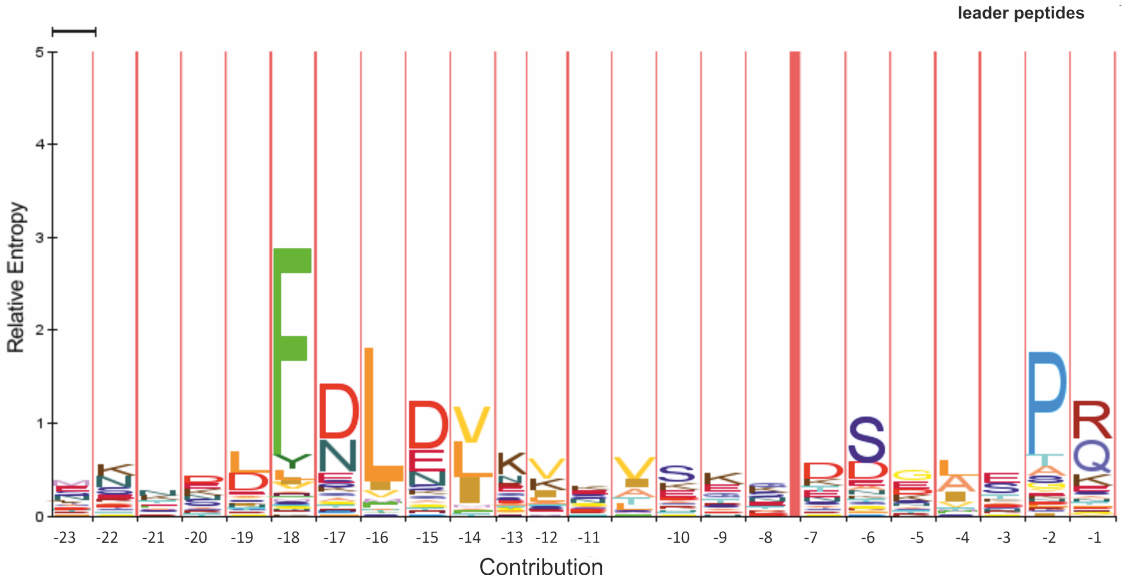
Figure S1. The HMM logos show the probability of each amino acid (height of the letter) and are scaled (width of the letter) according to how many sequences contributed to that position (i.e. narrow letters were generated from a smaller number of sequences than wider letters). The HMM logos were generated from 12 class I lantibiotic leader peptide sequences.



Accession numbers of the class I lantipeptides used for the generation of HMM-logos:

NisA P13068

NisZ P29559

Nisin Q BAD05046

Nisin F ABU45463

Nisin U Q2QBT0

Epilancin K7 AAA79236

Subtilin P10946

Pep5 CAA90023

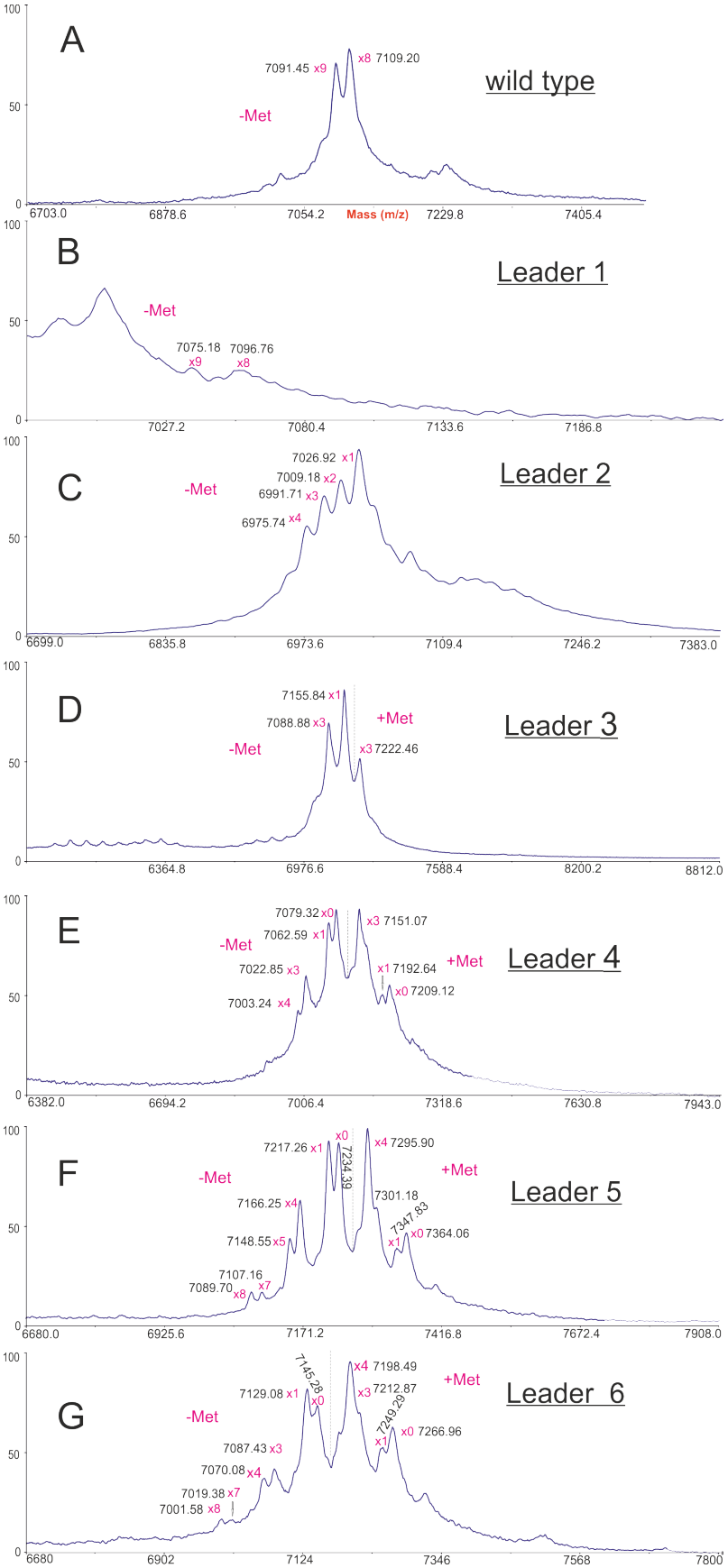
Ericin S AAL15569

Ericin A AAL15567

Epidermin P08136

Gallidermin P21838

Figure S2. Matrix-assisted laser desorption ionization–time-of-flight (MALDI-TOF) mass spectra of nisin variants modified *in vivo* by NisBTC enzymes in *L.lactis* and purified by Ni-NTA. –Met stands for nisin without the initial methionine, +Met stands for nisin with the initial methionine. x denotes the number of dehydrations.


A
wild type
7091.45 x9
x8 7109.20
-Met
100
50
0
6703.0
6878.6
7054.2
Mass (m/z)
7229.8
7405.4
B
Leader 1
-Met
7075.18
x9
7096.76
x8
7027.2
7080.4
7133.6
7186.8
C
Leader 2
-Met
7026.92 x1
7009.18 x2
6991.71 x3
6975.74 x4
6699.0
6835.8
6973.6
7109.4
7246.2
7383.0
D
Leader 3
7155.84 x1
7088.88 x3
+Met
-Met
x3 7222.46
6364.8
6976.6
7588.4
8200.2
8812.0
E
Leader 4
7079.32 x0
7062.59 x1
x3 7151.07
-Met
7022.85 x3
x1 7192.64
+Met
7003.24 x4
x0 7209.12
6382.0
6694.2
7006.4
7318.6
7630.8
7943.0
F
Leader 5
7217.26 x1
x0
7234.39
x4 7295.90
+Met
-Met
7166.25 x4
7301.18
7347.83
7148.55 x5
x1
x0 7364.06
7107.16
7089.70
x8
x7
6680.0
6925.6
7171.2
7416.8
7672.4
7908.0
G
Leader 6
7145.28
7129.08 x1
x0
x4 7198.49
x3 7212.87
+Met
-Met
7249.29
x1
x0 7266.96
7087.43 x3
7070.08 x4
7019.38 x7
7001.58 x8
6680
6902
7124
7346
7568
7800